

0400

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04/10/2001

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#2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/810,836

DATE: 03/30/2001
 TIME: 15:09:46

Input Set : A:\MBI0032.txt
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3 <110> APPLICANT: Broun, Pierre
 5 <120> TITLE OF INVENTION: Method for Modifying a Biosynthetic Pathway
 7 <130> FILE REFERENCE: MBI-0032
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/810,836
 C--> 9 <141> CURRENT FILING DATE: 2001-03-16
 9 <160> NUMBER OF SEQ ID NOS: 8
 11 <170> SOFTWARE: PatentIn version 3.0
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1239
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Arabidopsis thaliana
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (6)..(1091)
 21 <223> OTHER INFORMATION: G993
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 29 ctc tcc atc tct act act cca aag ccg aca acg acg gag aag aaa 98
 30 Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Glu Lys Lys
 31 20 25 30
 33 ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc 146
 34 Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
 35 35 40 45
 37 ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag 194
 38 Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
 39 50 55 60
 41 tca cgt aag ctt tcg tcg aaa tat aaa ggc gtt gtg cct cag cct 242
 42 Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
 43 65 70 75
 45 aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg 290
 46 Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
 47 80 85 90 95
 49 ctc ggt act ttc aac gag gaa gaa gct gcg tct tct tac gac atc 338
 50 Leu Gly Thr Phe Asn Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile
 51 100 105 110
 53 gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct 386
 54 Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser
 55 115 120 125
 57 caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct 434
 58 Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser
 59 130 135 140
 61 aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag 482
 62 Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu
 63 145 150 155
 65 ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct 530

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66 Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser				
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69 ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gca cgt				578
70 Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg				
71	180	185	190	
73 gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg				626
74 Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu				
75	195	200	205	
77 aac cgt tta gtt ata ccg aaa caa cac gca gag aag cat ttt ccg tta				674
78 Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu				
79	210	215	220	
81 ccg gca atg acg acg gca atg ggg atg aat ccg tct ccg acg aaa ggc				722
82 Pro Ala Met Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly				
83	225	230	235	
85 gtt ttg att aac ttg gaa gat aga aca ggg aaa gtt tgg cgg ttc cgt				770
86 Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg				
87 240	245	250	255	
89 tac agt tac tgg aac agc agt caa agt tac gtt ttg acc aag ggc tgg				818
90 Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp				
91	260	265	270	
93 agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtt gtt tgt				866
94 Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys				
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97 ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa				914
98 Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys				
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101 gtc cgg tct agt ccg gtt cag act gtt agg cta ttc gga gtc aac				962
102 Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn				
103	305	310	315	
105 att ttc aat gtt agt aac gag aaa cca aac gac gtc gca gta gag tgt				1010
106 Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys				
107 320	325	330	335	
109 gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt				1058
110 Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys				
111	340	345	350	
113 tcc aag aag cag gca att atc aac atc ttg tga caaattcttt tttttggtt				1111
114 Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu				
115	355	360		
117 tttttcttca atttttttctt cttttttcaa tattttgtat tgaaatgaca agttgtaaat				1171
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126 <212> TYPE: PRT				
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136 20 25 30
 139 Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
 140 35 40 45
 143 Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
 144 50 55 60
 147 Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
 148 65 70 75 80
 151 Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
 152 85 90 95
 155 Gly Thr Phe Asn Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
 156 100 105 110
 159 Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
 160 115 120 125
 163 Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys
 164 130 135 140
 167 Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
 168 145 150 155 160
 171 Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
 172 165 170 175
 175 Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
 176 180 185 190
 179 Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
 180 195 200 205
 183 Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
 184 210 215 220
 187 Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
 188 225 230 235 240
 191 Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
 192 245 250 255
 195 Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
 196 260 265 270
 199 Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
 200 275 280 285
 203 Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
 204 290 295 300
 207 Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
 208 305 310 315 320
 211 Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
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 228 <220> FEATURE:
 229 <221> NAME/KEY: CDS

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238 116
239 Met Asp
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241 ttt gac gag gag cta aat ctt tgt att acg aaa ggt aaa aat gtt gat 164
242 Phe Asp Glu Glu Leu Asn Leu Cys Ile Thr Lys Gly Lys Asn Val Asp
243 5 10 15
245 cat tct ttt gga gga gaa gct tct tcc acg tcc cca aga tct atg aag 212
246 His Ser Phe Gly Gly Glu Ala Ser Ser Thr Ser Pro Arg Ser Met Lys
247 20 25 30
249 aaa atg aag agt cct agt cgt cct aaa ccc tat ttc caa tcc tct tct 260
250 Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser Ser Ser
251 35 40 45 50
253 tct cct tat tcg tta gag gct ttc cct ttt tct ctc gat cca aca ctt 308
254 Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro Thr Leu
255 55 60 65
257 cag aat cag caa caa ctc gga tca tac gtt ccg gta ctt gag caa 356
258 Gln Asn Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu Glu Gln
259 70 75 80
261 cga caa gac ccg aca atg caa ggc cag aag caa atg atc tcc ttt agt 404
262 Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser Phe Ser
263 85 90 95
265 cct caa caa caa cag cag cag cag tat atg gcc cag tac tgg agt 452
266 Pro Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr Trp Ser
267 100 105 110
269 gac aca ttg aat ctg agt cca aga gga aga atg atg atg atg atg 500
270 Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met Ser
271 115 120 125 130
273 caa gaa gct gtt caa cct tac atc gca acg aag ctg tac aga gga gtg 548
274 Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg Gly Val
275 135 140 145
277 aga caa cgt caa tgg gga aaa tgg gtc gca gag atc cgt aag cca cga 596
278 Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys Pro Arg
279 150 155 160
281 agc agg gca cgt ctt tgg ctt ggt acc ttt gat aca gct gaa gaa gct 644
282 Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala
283 165 170 175
285 gcc atg gcc tac gac cgc caa gcc ttc aaa tta cga ggc cac agc gca 692
286 Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His Ser Ala
287 180 185 190
289 aca ctg aat ttc ccg gag cat ttt gtg aat aag gaa agc gag ctg cat 740
290 Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu Leu His
291 195 200 205 210
293 gat tca aac tcg tcg gat cag aaa gaa cct gaa acg cca cag cca agc 788
294 Asp Ser Asn Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln Pro Ser
295 215 220 225

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297 gag gtt aac ttg gag agc aag gaa cta ccg gtg att gat gtt ggg aga	836
298 Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val Gly Arg	
299 230 235 240	
301 gag gaa ggt atg gct gag gca tgg tac aat gcc att aca tcg gga tgg	884
302 Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser Gly Trp	
303 245 250 255	
305 ggt cct gaa agt cct ctt tgg gat gat ttg gat agt tct cat cag ttt	932
306 Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His Gln Phe	
307 260 265 270	
309 tca tca gaa agc tca tct tct cct ctc tct tgt cct atg agg cct	980
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311 275 280 285 290	
313 ttc ttt tga aaaagtttat aaacccacat tgtgtttag gttatagttt	1029
314 Phe Phe	
317 agggttatgc tcattggcat ttggatggag gcaatttttgc tgatctccca ttccaccaca	1089
319 tatacgtcat tataatgtgtc tacctttctt ctgtattttctt atcattatca ttgttttttat	1149
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342 35 40 45	
345 Ser Ser Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro	
346 50 55 60	
349 Thr Leu Gln Asn Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu	
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353 Glu Gln Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser	
354 85 90 95	
357 Phe Ser Pro Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr	
358 100 105 110	
361 Trp Ser Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met	
362 115 120 125	
365 Met Ser Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg	
366 130 135 140	
369 Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys	
370 145 150 155 160	
373 Pro Arg Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu	
374 165 170 175	
377 Glu Ala Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His	
378 180 185 190	
381 Ser Ala Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu	
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/810,836

DATE: 03/30/2001

TIME: 15:09:47

Input Set : A:\MBI0032.txt

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date